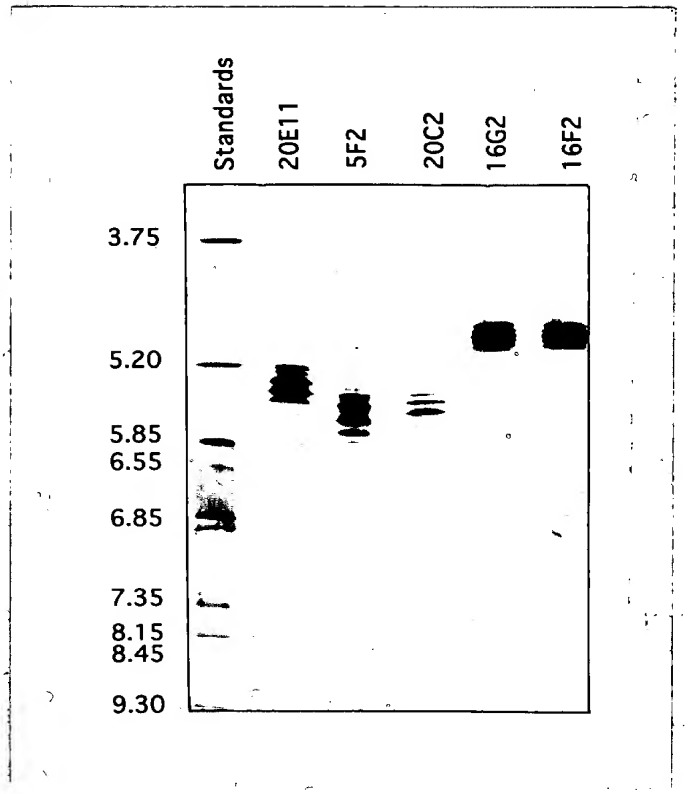
Standards
20E11
5F2
20C2
16G2
16F2
3.75
5.20
5.85
6.55
6.85
7.35
8.15
8.45
9.30

FIG. 2

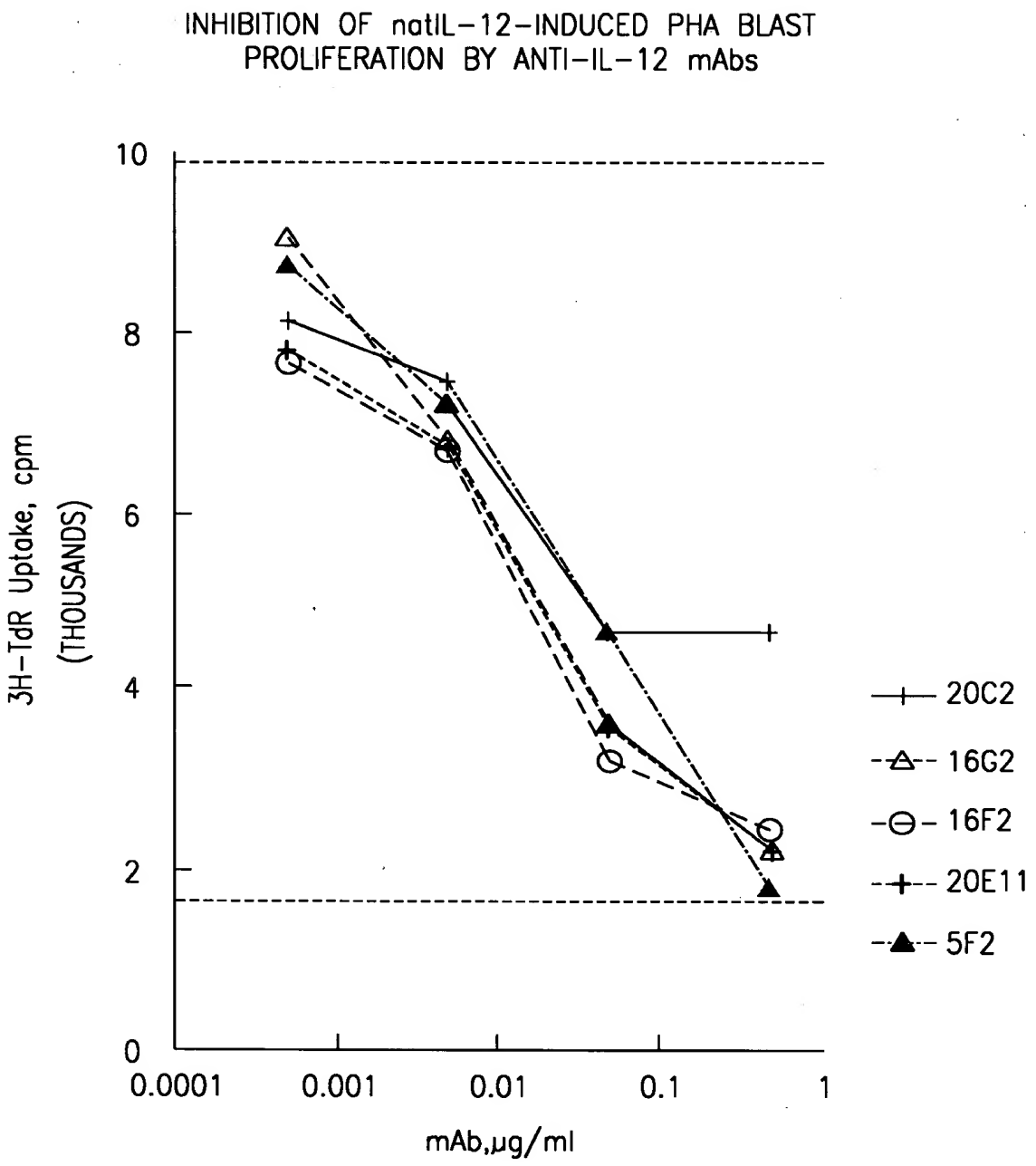
INHIBITION OF natIL-12-INDUCED PHA BLAST PROLIFERATION BY ANTI-IL-12 mAbs
3H-TdR Uptake, cpm (THOUSANDS)
10
8
6
4
2
0
0.0001
0.001
0.01
0.1
1
mAb,µg/ml
20C2
16G2
16F2
20E11
5F2

*FIG. 3*

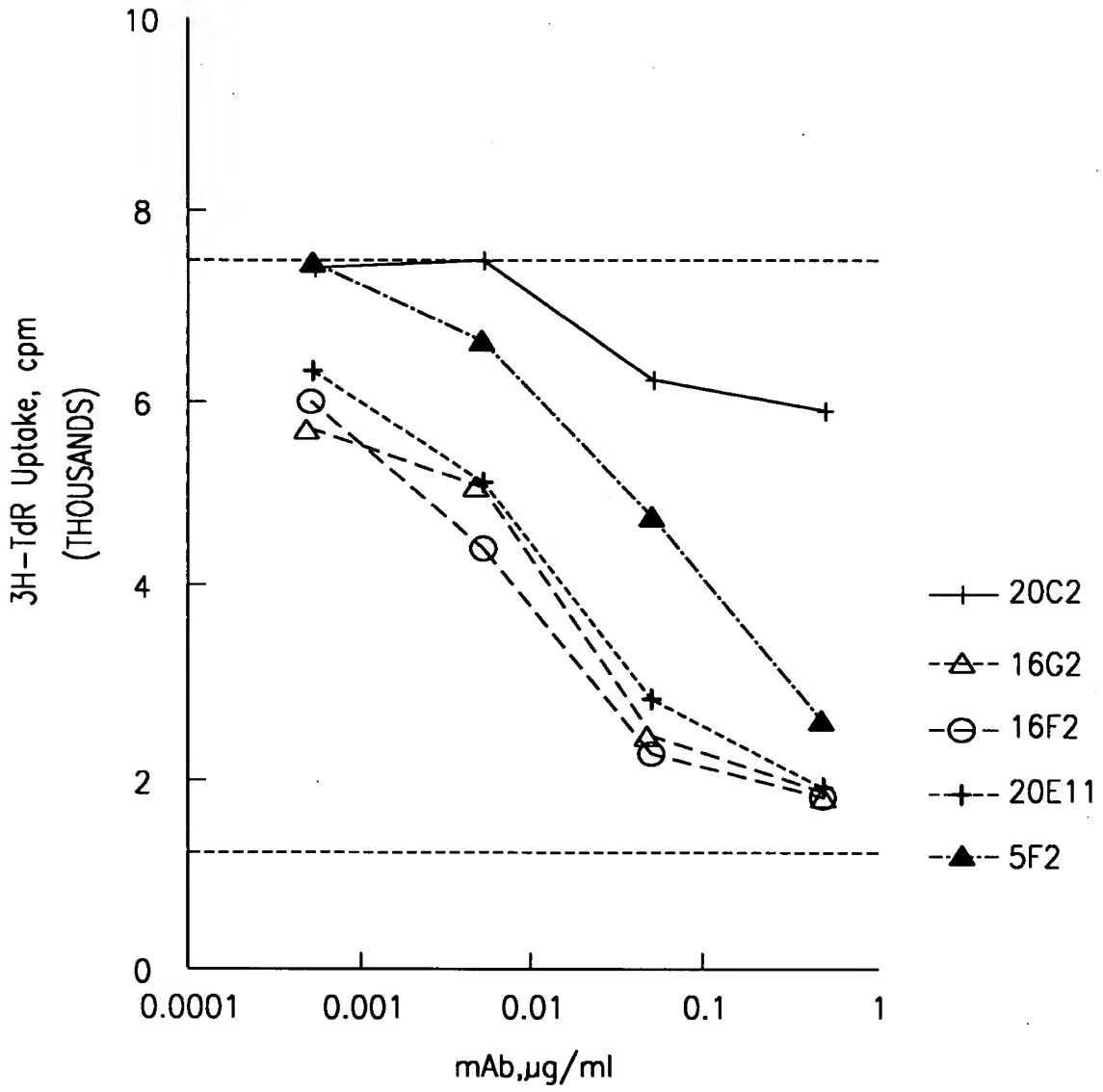
INHIBITION OF RHESUS IL-12-INDUCED PHA BLAST PROLIFERATION BY ANTI-IL-12 mAbs
3H-TdR Uptake, cpm (THOUSANDS)
10
8
6
4
2
0
0.0001
0.001
0.01
0.1
1
mAb,µg/ml
20C2
16G2
16F2
20E11
5F2

*FIG. 4*

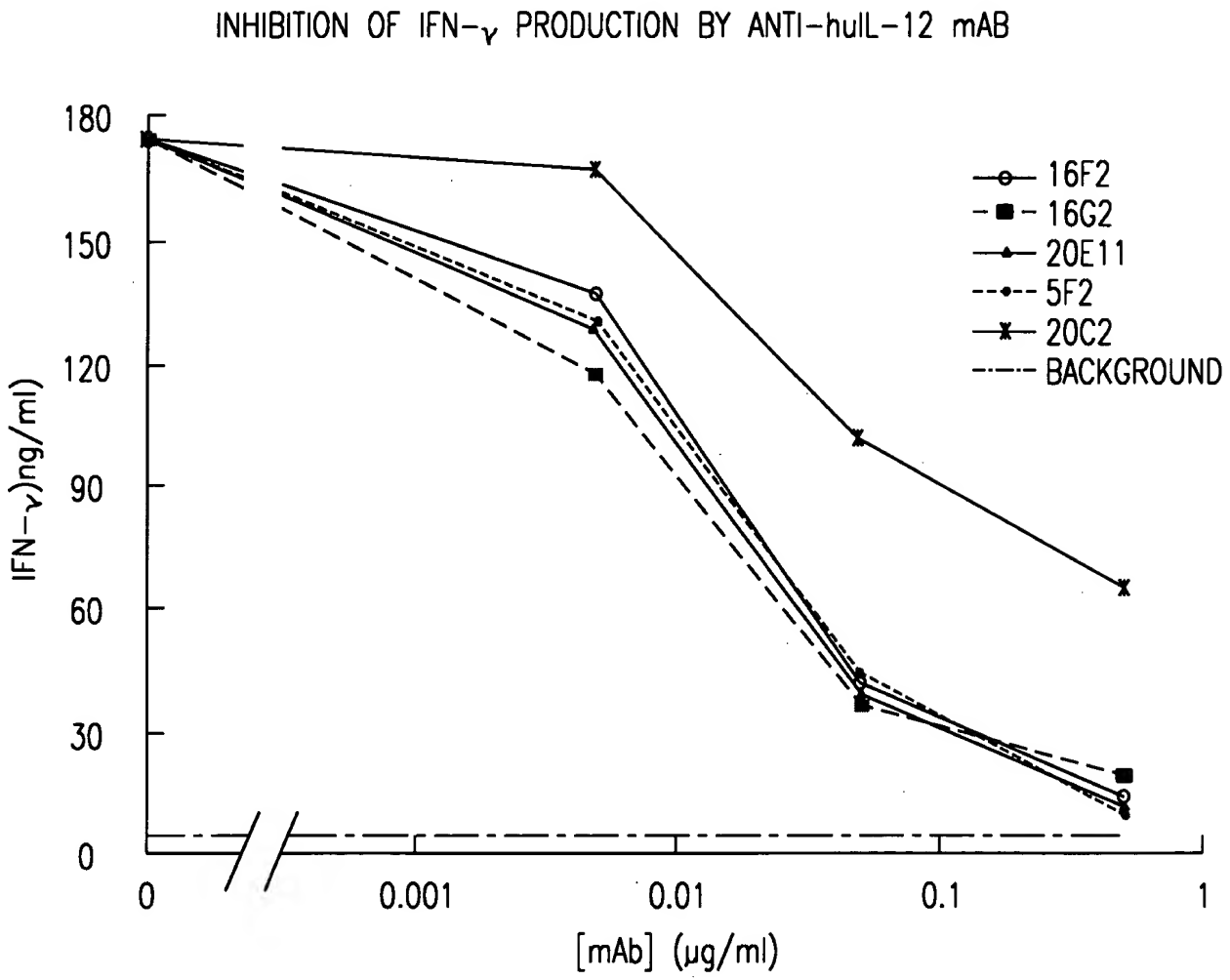
INHIBITION OF IFN-γ PRODUCTION BY ANTI-hulL-12 mAB
180
150
120
90
60
30
0
IFN-γ)ng/ml)
0
0.001
0.01
0.1
1
[mAb] (μg/ml)
16F2
16G2
20E11
5F2
20C2
BACKGROUND

FIG. 5

16G2 HEAVY CHAIN VARIABLE REGION

```
                                                  27                                                  54
CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC ACC
GAC CTC CTC AGT CCT GGA TCG GAG CAC TT  GGA AGA GTC TGA GAC AGG GAG TGG
LeuGluGluSerGlyProSerLeuValLysPro SerGlnThr LeuSerLeuThr

                                                  81                                                 108
TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG ATC CGG AAA
ACA AGA CAG TGA CCG CTG AGG TAG TGG TCA CCA ATG ACC TTG ACC TAG GCC TT
CysSerValThrGlyAspSerIleThrSerGly TyrTrpAsnTrpIleArgLys

                                                 135                                                 162
TTC CCA GG  AAT AAA TT  GAG TAC ATG GGA TTC  ATA AGT TAT AGT GGT AGC ACT
AAG GGT CCC TTA TT  AAA CTC ATG TAC CCT AAG ATA TCA ATA TCA CCA TCG TGA
Ph  ProGlyAsnLysPh  GluTyr MET GlyPheIleSerTyrSerGlySerThr

                                                 189                                                 216
TAC AAT ATT CCA TCT CTC AAA AAT CGA GTC TCC  ATC ACT CGA GAC ACA TCC AAT
ATG TTA TTA GGT AGA GAG TT  TTA GCT CAG AGG  TAG TGA GCT CTG TGT AGG TTA
TyrAsnAsnProSerLeuLysAsnArg ValSer IleThrArgAspTThSerAsn

                                                 243                                                 270
AAC CAG TAC TAC CTG CAG TTG AGT TCT GTG ACT  ACT GAG GAC TCA GCC ACA TAT
TTG GTC ATG ATG GAC GTC AAC TCA AAG CAC TGA  TGA CTC CTG AGT CGG TGT ATA
AsnGlnTyr TyrLeuGlnLeuSerSerVal Thr ThrGluAspSerAlaThrTyr

                                                 297
TAC TGT GCA AGA TCT TCG GAT GCT TTG GAC TAC  TGG GGC CGA GG  ACC ACG
ATG ACA CGT TCT AGA AGC CTA CGA AAC CTG ATG  ACC CCG CGT CCC TGG TGC
TyrCysAlaArgSerSerAspAlaLeuAspTyr TrpGlyAlaGlyThrThr
```

*FIG. 6*

20E11 HEAVY CHAIN VARIABLE REGION

```
                                                  27                                                  54
GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT  TCT CAG ACT CTG TCC CTC ACC TGT
CTC CTC AGT CCT GGA TCG GAG CAC T T  GGA AGA GTC TGA GAC AGG GAG TGG ACA
Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys

                                                  81                                                 108
TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC  TGG AAC TGG ATC CGG AAA TTC
AGA CAG TGA CCG CTG AGG TAG TGG TCA CCA ATG  ACC TTG ACC TAG GCC T T  AAG
Ser Val Thr Gly Asp Ser Ile  Thr Ser Gly Tyr Trp Asn Trp Ile Arg Lys Pne

                                                 135                                                 162
CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA  AGT TAC AGT GGT AGT ACT TAC
GGT CTA TTA TGT GAA CTC ATG TAC CCT ATG TAT  TCA ATG TCA CCA TCA TGA ATG
Pro Asp Asn Thr Leu Glu Tyr MET Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Tyr

                                                 189                                                 216
TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC ATC  ACT CGA GAC ACA TCC AAG AAC
ATG TTA GGT AGA GAG TCT TCA GCT TAG AGG TAG  TGA GCT CTG TGT AGG TTC TTG
Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn

                                                 243                                                 270
CGA TAC TCC ATG CAG TTG AAT TCT GTG ACT ACT  GAG GAC ACA GCC ACA TAT TAC
GTC ATG AGG TAC GTC AAC TTA AGA CAC TGA TGA  CTC CTG TGT CGG TGT ATA ATG
Gln Tyr Ser MET Gln Leu Asn Ser Val Thr Thr  Glu Asp Thr Ala Thr Tyr Tyr

                                                 297
TGT GCA AGA TCC TCG GAT GCT ATG GAC TAC TGG GGC GC
ACA CGT TCT AGG AGC CTA CGA TAC CTG ATG ACC CCG CG
Cys Ala Arg Ser Ser Asp Ala MET Asp Tyr Trp Gly
```

*FIG. 7*